## CLAIM AMENDMENT

Please amend the claims as indicated below:

1. (Currently amended) An isolated nucleic acid sequence comprising a cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter, wherein the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter comprises:

(a) a nucleic acid sequence of SEQ ID NO:18 or a fragment thereof, having promoter activity, wherein the fragment comprises from 400 to 2547 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:18; or

(b) a nucleic acid sequence comprising from 400 to 2547 contiguous nucleotides that hybridizes to the nucleic acid sequence of SEQ ID NO:18 under wash conditions of 2X SCP, 1% SDS at 65°C for 30 minutes.

2-3. (Cancelled)

4. (Original) The isolated nucleic acid of claim 1, wherein the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter comprises from 750 to 2547 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:18.

5. (Original) The isolated nucleic acid of claim 1, wherein the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter comprises from 1000 to 2547 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:18.

6. (Original) The isolated nucleic acid of claim 1, wherein the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter comprises from 1500 to 2547 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:18.

7. (Original) The isolated nucleic acid of claim 1, wherein the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter comprises from 1750 to 2547 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:18.

8. (Original) The isolated nucleic acid of claim 1, wherein the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter comprises from 2000 to 2547 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:18.

9. (Original) The isolated nucleic acid of claim 1, wherein the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter comprises from 2250 to 2547 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:18.

10. (Original) The isolated nucleic acid of claim 1, wherein the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter comprises from 2500 to 2547 contiguous nucleotides of the nucleic acid sequence of SEQ ID NO:18.

11. (Original) The isolated nucleic acid of claim 1, wherein the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter comprises the nucleic acid sequence of SEQ ID NO:18, or a fragment thereof comprising promoter activity.

12. (Original) The isolated nucleic acid of claim 1, further comprising an enhancer.

13. (Previously presented) The isolated nucleic acid of claim 12, wherein the enhancer comprises an intron.

14. (Original) The isolated nucleic acid of claim 13, wherein the intron is selected from the group consisting of the rice actin 1 intron and the rice actin 2 intron.

15. (Original) The isolated nucleic acid of claim 1, further comprising a 3' UTR.

16. (Original) The isolated nucleic acid of claim 15, wherein the 3' UTR comprises a *PIN II* 3' UTR.

17. (Previously presented) A transgenic plant stably transformed with a selected DNA comprising the cytoplasmic glutamine synthetase $GS_{1-2}$ promoter of claim 1 operably linked to a selected heterologous coding region.

18. (Original) The transgenic plant of claim 17, wherein the selected heterologous coding region encodes a protein imparting insect resistance, bacterial disease resistance, fungal disease resistance, viral disease resistance, nematode disease resistance, herbicide resistance, nutrient transporter functions, enhanced grain composition or quality, enhanced nutrient utilization, enhanced environment or stress resistance, reduced mycotoxin contamination, female sterility, a selectable marker phenotype, a screenable marker phenotype, a negative selectable marker phenotype, or altered plant agronomic characteristics.

19. (Original) The transgenic plant of claim 18, wherein the selected heterologous coding region encodes a protein imparting a selectable marker phenotype, wherein the protein is selected from the group consisting of phosphinothricin acetyltransferase, glyphosate resistant EPSPS, aminoglycoside phosphotransferase, hygromycin phosphotransferase, neomycin phosphotransferase, dalapon dehalogenase, bromoxynil resistant nitrilase, anthranilate synthase and glyphosate oxidoreductase.

20. (Original) The transgenic plant of claim 17, wherein the selected heterologous coding region is operably linked to a 3' UTR.

21. (Original) The transgenic plant of claim 20, wherein the 3' UTR is a *pinII* 3' UTR.

22. (Original) The transgenic plant of claim 17, wherein the selected DNA comprises an enhancer.

23. (Original) The transgenic plant of claim 22, wherein the enhancer is selected from the group consisting of rice actin 1 intron and rice actin 2 intron.

24. (Original) The transgenic plant of claim 17, wherein the selected DNA comprises plasmid DNA.

25. (Original) The transgenic plant of claim 17, wherein the selected DNA comprises a sequence encoding a signal peptide.

26. (Original) The transgenic plant of claim 25, wherein the signal peptide comprises a chloroplast transit peptide.

27. (Original) The transgenic plant of claim 17, comprising a sequence encoding a transit peptide, wherein the transit peptide is selected from the group consisting of chlorophyll a/b binding protein transit peptide, small subunit of ribulose bisphosphate carboxylase transit peptide, EPSPS transit peptide and dihydrodipocolinic acid synthase transit peptide.

28. (Original) The transgenic plant of claim 17, further defined as a monocotyledonous plant.

29. (Original) The transgenic plant of claim 28, wherein the monocotyledonous plant is selected from the group consisting of wheat, maize, rye, rice, oat, barley, turfgrass, sorghum, millet and sugarcane.

30. (Original) The transgenic plant of claim 29, wherein the monocotyledonous plant is maize.

31. (Original) The transgenic plant of claim 17, further defined as a dicotyledonous plant.

32. (Original) The transgenic plant of claim 31, wherein the dicotyledonous plant is selected from the group consisting of tobacco, tomato, potato, soybean, cotton, canola, alfalfa, sunflower, and cotton.

33. (Original) The transgenic plant of claim 32, wherein the dicotyledonous plant is a soybean plant.

34. (Original) The transgenic plant of claim 17, further defined as a fertile $R_0$ transgenic plant.

35. (Original) A seed of the fertile $R_0$ transgenic plant of claim 34, wherein the seed comprises the selected DNA.

36. (Original) The transgenic plant of the claim 17, further defined as a progeny plant of any generation of a fertile $R_0$ transgenic plant.

37. (Original) A seed of the progeny plant of claim 36, wherein the seed comprises the selected DNA.

38. (Previously presented) A crossed fertile transgenic plant prepared according to the method comprising the steps of:

(i) obtaining a fertile transgenic plant comprising a selected DNA comprising the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter of claim 1;

(ii) crossing the fertile transgenic plant with itself or with a second plant to prepare the seed of a crossed fertile transgenic plant, wherein the seed comprises the selected DNA; and

(iii) planting the seed to obtain a crossed fertile transgenic plant.

39. (Original) The crossed fertile transgenic plant of claim 38, wherein the second plant lacks the selected DNA.

40. (Original) A seed of the crossed fertile transgenic plant of claim 38, wherein the seed comprises the selected DNA.

41. (Original) The crossed fertile transgenic plant of claim 38, further defined as a monocotyledonous plant.

42. (Original) The crossed fertile transgenic plant of claim 41, wherein the monocotyledonous plant is selected from the group consisting of wheat, oat, barley, maize, rye, rice, turfgrass, sorghum, millet and sugarcane.

43. (Original) The crossed fertile transgenic plant of claim 42, wherein the monocotyledonous plant is a maize plant.

44. (Original) The crossed fertile transgenic plant of claim 38, further defined as a dicotyledonous plant.

45. (Original) The crossed fertile transgenic plant of claim 44, wherein the dicotyledonous plant is selected from the group consisting of tobacco, tomato, potato, soybean, canola, alfalfa, sunflower and cotton.

46. (Original) The crossed fertile transgenic plant of claim 45, wherein the dicotyledonous plant is a soybean plant.

47. (Original) The crossed fertile transgenic plant of claim 38, wherein the selected DNA is inherited through a female parent.

48. (Original) The crossed fertile transgenic plant of claim 38, wherein the selected DNA is inherited through a male parent.

49. (Original) The crossed fertile transgenic plant of claim 38, wherein the second plant is an inbred plant.

50. (Original) The crossed fertile transgenic plant of claim 49, wherein the crossed fertile transgenic plant is a hybrid.

51. (Original) The crossed fertile transgenic plant of claim 38, wherein the selected DNA comprises a selected heterologous coding region operably linked to the maize cytoplasmic glutamine synthetase $GS_{1-2}$ promoter.

52. (Original) The crossed fertile transgenic plant of claim 51, wherein the selected coding region encodes a protein selected from the group consisting of a protein imparting insect resistance, bacterial disease resistance, fungal disease resistance, viral disease resistance, nematode disease resistance, herbicide resistance, nutrient transporter functions, enhanced grain composition or quality, enhanced nutrient utilization, enhanced environment or stress resistance, reduced mycotoxin contamination, female sterility, a selectable marker phenotype, a screenable marker phenotype, a negative selectable marker phenotype, or altered plant agronomic characteristics.

53. (Original) The crossed fertile transgenic plant of claim 38, wherein the selected DNA comprises an enhancer.

54. (Original) The crossed fertile transgenic plant of claim 53, wherein the enhancer is selected from the group consisting of rice actin 1 intron and rice actin 2 intron.

55. (Original) The crossed fertile transgenic plant of claim 51, wherein the selected coding region is operably linked to a 3' UTR.

56. (Original) The crossed fertile transgenic plant of claim 55, wherein the 3' UTR is a *pinII* 3' UTR.

57. (Previously presented) A method of preparing a transgenic plant comprising the steps of:

(i) obtaining a construct comprising the cytoplasmic glutamine synthetase $GS_{1-2}$ promoter of claim 1;

(ii) transforming a recipient plant cell with the construct; and

(iii) regenerating the recipient plant cell to obtain a transgenic plant transformed with the construct.

58. (Original) The method of claim 57, wherein the maize cytoplasmic glutamine synthetase $GS_{1-2}$ promoter is operably linked to a selected coding region.

59. (Original) The method of claim 57, wherein the transgenic plant is fertile.

60. (Original) The method of claim 59, further comprising the step of obtaining seed from the fertile transgenic plant.

61. (Original) The method of claim 60, further comprising obtaining a progeny plant of any generation from the fertile transgenic plant.

62. (Original) The method of claim 57, wherein the step of transforming comprises a method selected from the group consisting of microprojectile bombardment, PEG mediated transformation of protoplasts, electroporation, silicon carbide fiber mediated transformation, or *Agrobacterium*-mediated transformation.

63. (Original) The method of claim 62, wherein the step of transforming comprises microprojectile bombardment.

64. (Original) The method of claim 57, wherein the recipient plant cell is from a monocotyledonous plant.

65. (Original) The method of claim 64, wherein the monocotyledonous plant is selected from the group consisting of wheat, maize, rye, rice, turfgrass, oat, barley, sorghum, millet, and sugarcane.

66. (Original) The method of claim 65, wherein the monocotyledonous plant is a maize plant.

67. (Original) The method of claim 57, wherein the recipient plant cell is from a dicotyledonous plant.

68. (Original) The method of claim 67, wherein the dicotyledonous plant is selected from the group consisting of tobacco, tomato, potato, soybean, canola, sunflower, alfalfa and cotton.

69. (Original) The method of claim 58, wherein the selected coding region encodes a protein imparting insect resistance, bacterial disease resistance, fungal disease resistance, viral disease resistance, nematode disease resistance, herbicide resistance, nutrient transporter functions, enhanced grain composition or quality, enhanced nutrient utilization, enhanced environment or stress resistance, reduced mycotoxin contamination, female sterility, a selectable marker phenotype, a screenable marker phenotype, a negative selectable marker phenotype, or altered plant agronomic characteristics.

70. (Original) The method of claim 57, wherein the construct comprises an enhancer.

71. (Original) The method of claim 70, wherein the enhancer is selected from the group consisting of rice actin 1 intron and rice actin 2 intron.

72. (Original) The method of claim 58, wherein the selected coding region is operably linked to a 3' UTR.

73. (Original) The method of claim 72, wherein the 3' UTR is a *pinII* 3' UTR.

74. (Previously presented) A method of plant breeding comprising the steps of:

(i) obtaining a transgenic plant comprising a selected DNA comprising the cytoplasmic glutamine synthetase $GS_{1\text{-}2}$ promoter of claim 1; and

(ii) crossing the transgenic plant with itself or a second plant.

75. (Original) The method of claim 74, wherein the transgenic plant is a monocotyledonous plant.

76. (Original) The method of claim 75, wherein the monocotyledonous plant is selected from the group consisting of wheat, maize, oat, barley, rye, rice, turfgrass, sorghum, millet and sugarcane.

77. (Original) The method of claim 76, wherein the monocotyledonous plant is a maize plant.

78. (Original) The method of claim 74, wherein the transgenic plant is a dicotyledonous plant.

79. (Original) The method of claim 78, wherein the dicotyledonous plant is selected from the group consisting of tobacco, tomato, potato, soybean, canola, sunflower, alfalfa and cotton.

80. (Original) The method of claim 74, wherein the transgenic plant is crossed with the second plant.

81. (Original) The method of claim 80, wherein the second plant is an inbred plant.

82. (Original) The method of claim 74, further comprising the steps of:

(iii) collecting seeds resulting from the crossing;

(iv) growing the seeds to produce progeny plants;

(v) identifying a progeny plant comprising the selected DNA; and

(vi) crossing the progeny plant with itself or a third plant.

83. (Original) The method of claim 82, wherein the progeny plant inherits the selected DNA through a female parent.

84. (Original) The method of claim 82, wherein the progeny plant inherits the selected DNA through a male parent.

85. (Original) The method of claim 82, wherein the second plant and the third plant are of the same genotype.

86. (Original) The method of claim 85, wherein the second and third plants are inbred.

87. (Original) The method of claim 74, wherein the selected DNA further comprises a coding region, wherein the coding region encodes a protein imparting insect resistance, bacterial disease resistance, fungal disease resistance, viral disease resistance, nematode disease resistance, herbicide resistance, nutrient transporter functions, enhanced grain composition or quality, enhanced nutrient utilization, enhanced environment or stress resistance, reduced mycotoxin contamination, female sterility, a selectable marker phenotype, a screenable marker phenotype, a negative selectable marker phenotype, or altered plant agronomic characteristics.

88. (Original) The method of claim 74, wherein the selected DNA further comprises a genetic element which enhances the expression of the protein in the transgenic plant.

89. (Original) The method of claim 88, wherein the genetic element is selected from the group consisting of the rice actin 1 intron and the rice actin 2 intron.